5

Evaluation of Method Variation

The purpose of this chapter is to address issues related to method rigor and the effect of different levels of rigor on assessment results. A critical factor in selecting the level of application of RBPs is the availability of tiers. RBPI, II, and III represent three levels of intensity with RBPI being the most rapid and least rigorous (Plafkin et al. 1989). RBPI is based only on field observation of benthic invertebrates without any standardized sampling effort or index/metric calculations and interpretations. RBPII and RBPIII employ standardized sampling gear and effort, field and laboratory taxonomic identification, respectively, and subsampling. Decisions on which of these protocols to use are usually focused on some combination of these components in the context of protocol sensitivity and resource availability (Ferraro et al. 1989; Ferraro and Cole 1992). The analyses below are designed to evaluate the effects of subsample size and taxonomic level on metric performance and overall assessment results; these comparisons were conducted only for the New York case study. Though the results here might produce some conclusions on methods, it should be realized that these comparisons will not necessarily apply to other regions of the country.

5.1 Adequacy of Screening Level (Rapid Bioassessment Protocol)

RBPI screening level assessments are based on the relative abundance of organisms collected at a site. Collection of macroinvertebrates consists of turning over rocks (hand picking) and/or taking qualitative samples with a dipnet. These samples are supplemented by field examinations of periphyton, macrophytes, slimes, and fish which provide additional information for determining presence or absence of degradation. The variety of organisms (taxa richness), their relative tolerance levels, and factors observed for other biota, are then used to determine if the site is impaired. The adequacy of this approach relies on three basic factors: (1) that the assessment needed provides only the presence or absence of degradation, not detailed information as to the nature and cause of the degradation, (2) that the individual performing the assessment has a strong familiarity with aquatic invertebrate taxonomy generally at family-level, and (3) that the individual has knowledge of or access to information on relative pollution tolerance and functional feeding group associations of different aquatic biota.

The assessments produced by this screening level effort are presented in Table 5-1. These results did show sampling stations where there was impaired biological condition (Table 5-1). Most of the screening level assessments fell within the range of the higher level assessment (Table 5-2).

This screening level of assessment did underestimate impairment on one occasion, station CHR4, the initial regional reference site for Canastota and Harbor Brook that was dropped after further assessment. The screening level assessment notes the relative abundance and variety of organisms observed. The categories of abundance are:

- Rare <3
- Common 3-9
- Abundant >10
- Dominant >50 (estimate).

Initial assessment of station CHR4 showed a good variety of sensitive organisms (e.g., Plecoptera, Ephemeroptera-dominant). However, with such a rating system, the hyper-abundant Amphipola was given the same rating, i.e., dominant. Further evaluation of CHR4 using RBPIII level assessment revealed that Gammarus (Amphipoda: Gammaridae) comprised ~76 percent of the sample thus indicating impairment of the aquatic community. Overall, however, the RBPI is an adequate and cost-effective screening level assessment.

5.2 Metric Performance with Variable Methods

The different assessment levels of RBPs provide a means for agencies to tailor their biological monitoring programs to suit

Table 5-1 Narrative screening-level assessments (RBPI) of 10 study stations in New York State performed 20-23 September 1993. Use of narratives for impairment is based on the following categories of *increasing* biological degradation or impairment: minimal-slight-moderate-severe.

STATION	IMPAIRMENT	REASON(S) FOR ASSESSMENT
CC1	slight to moderate	1. Dominance of relatively tolerant Hydropsychidae (net-spinning caddisflies) and Elmidae (riffle beetles). 2. Heavy embeddedness of substrate, some upstream bank instability. 3. Narrow buffer zone, both sides. 4. Potential organic enrichment from agricultural operations.
CC2	moderate	1. Dominance of Hydropsychidae and Elmidae (both relatively tolerant); abundant Oligochaeta (aquatic earthworms). 2. Substrate almost completely sand and some small gravel. 3. Considerable upstream bank instability. 4. Removal of canopy on one side. 5. Abundant growths of blue-green and filamentous green algae on substrate. 6. Habitat degradation and organic enrichment.
CC3	moderate	1. Dominance of Hydropsychidae and Elmidae; Oligochaeta and Chironomidae (midges) common. 2. Substrate almost completely composed of sand and small gravel. 3. Severe bank instability. 4. Narrow buffer zones on both sides; agricultural fields within 5-7 meters on both sides. 5. Habitat degradation, organic enrichment, potential highway and agricultural runoff problems.
HB1	moderate	1. Dominance of Amphipoda (scud), Chironomidae and Hydropsychidae, all relatively tolerant. 2. Some embeddedness as evidence of upstream erosion. 3. Narrow vegetated buffer zone, both sides; little or no canopy cover. 4. Abundant growths of filamentous green and blue-green algae, and mosses. 5. Habitat degradation, organic enrichment, potential toxicants.
HB2	severe	1. Dominance of Amphipoda and Chironomidae, both considered relatively tolerant; Oligochaeta and Physidae abundant. 2. Copepoda, normally inhabiting standing waters, abundant. 3. Extreme habitat modification, channelized, stone walls, very low current velocity, deep, no riffles. 4. Habitat degradation, organic enrichment, potential toxicants.
HB3	severe	1. Dominance of Gastropoda (probably physidae), Chironomidae, and Hirundinea, all considered tolerant. 2. Extreme habitat modification, channelized, stone walls, low current velocity, deep, no riffles, silty/muck bottom with macrophytes. 3. Habitat degradation, organic enrichment, potential toxicants.
CHR4	minimal	1. Hyper-dominance of Amphipoda outweighed by considerable diversity of taxa recognized as relatively pollution-sensitive including Ephemeroptera (mayflies), Plecoptera (stoneflies), and Trichoptera (caddisflies) (several families of the latter). 2. High-gradient, no upstream habitat degradation/modification. 3. Dominant growths of epilithic mosses and some filamentous green algae, potential for minor organic enrichment.
OC1	moderate	1. Dominance of Oligochaeta and Chironomidae, both relatively tolerant of both physical and chemical disturbances. 2. Ephemeroptera, Plecoptera, and Coleoptera, each with a mixture of tolerant and intolerant species, considered common. 3. Channelized, uniform habitat, embedded substrate, lack of riparian vegetation. 4. Potential organic enrichment.

Table 5-1 (continued).

STATION	IMPAIRMENT	REASON(S) FOR ASSESSMENT
OC2	moderate to severe	1. Dominance of Hydropsychidae, exhibits strongly positive response to organic enrichment and tolerance to some physical degradation. 2. Amphipoda, Oligochaeta, and Chironomidae considered abundant; all are tolerant. 3. Channelized with mortared stone walls, and considerable accumulation of gravel and cobble; minimal riparian vegetation. 4. Likely receiving considerable organic inputs.
OC3	moderate to severe	1. Dominance of Oligochaeta. 2. Planaria, Hirudinea, Amphipoda, Hydropsychidae, and Chironomidae considered abundant-all pollution-tolerant forms. 3. Channelized, very narrow riparian zone, heavy urban development on both sides, much coarse human trash and other debris. 4. Strong sewage odor. 5. Likely receiving heavy organic inputs combined with other urban runoff.
OC4	slight	1. Dominance of Trichoptera (several families) and Elmidae; some sub-taxa can be positively responsive to organic enrichment. 2. Hydracarina, Ephemeroptera (several families), and Chironomidae considered abundant; some taxa are sensitive, others are tolerant. 3. Good substrate diversity and riparian vegetation with canopy. 4. Some potential for asphalt runoff and a mixture of slight organic enrichment combined with low-level toxicants.

their needs. RBPI is used as an initial screening level assessment for many sites. If an impaired biological condition is noted, further assessment may be carried out with RBPII (family level taxonomy) or RBPIII (genus/species level taxonomy). The study was designed to compare results from RBPII with RBPIII. RBPII requires specimen identification no finer than to family level, whereas RBPIII uses "the lowest practical taxonomic level" (Plafkin et al. 1989), generally genus or species level. Therefore, to address the questions related to level of taxonomic identification, two datasets, one based on family-level taxonomy and one based on genus/species level, were needed. Results received from the laboratory were generally at the genus or species level (Appendix B). For a family-level dataset, taxa were combined under the family name and the number of individuals for each family was summed.

In order to evaluate sample size, it was necessary to calculate metrics and develop scoring criteria based on both the 100-organism and 300-organism subsamples. Data sets representing the latter were obtained by combining the data from 100- and 200-organism subsamples for each sampling station.

Metric values calculated based on 300-organism subsamples with genus/species-level taxonomy are presented in Table 4-3. The metric values to which these are compared are based on (1) family-level identification of 100-organism subsamples (Table 5-3) and (2) genus-level identification of 100-organism subsamples (Table 5-4).

5.2.1 Taxonomic Level Effects on Metric Performance

The level of taxonomy used for a biological assessment depends on the program objectives and resources. Biological assessment results may not vary substantially between family versus genus/species level taxonomy, however, interpretation of results may be problematic at the family (or higher) level. If broad-scale status analyses are desired for a large number of sites, RBPII assessment level may be adequate. If, for example, causal relationships need to be identified, RBPIII would be a better alternative potentially giving greater sensitivity.

Using the metric values calculated on 100-organism subsamples, comparisons of the effect of taxonomic level were made based on (1) performance of single metrics and (2) total bioassessment score. For both, correlation scatterplots were developed that illustrate the relationship between these measures at a single sampling station when differential taxonomic resolution is used. At the family level of identification, we would expect a smaller number of groupings with a larger number of individuals than is

Table 5-2 Comparison of biological assessments between RBPI and RBPIII

STATION	RBPI ASSESSMENT	RBPIII ASSESSMENT
CC1	slight to moderate	slight to moderate
CC2	moderate	slight to moderate
CC3	moderate	moderate
HB1	moderate	moderate
HB2	severe	severe
HB3	severe	*
CHR4	minimal	severe
OC1	moderate	moderate
OC2	moderate to severe	moderate to severe
OC3	moderate to severe	moderate to severe
OC4	slight	slight

*no further assessment was conducted on this site due to severe habitat alterations.

expected with genus/species-level taxonomy. Perfect (1:1) agreement between the metric values at a single station with different taxonomic levels will be reflected by a point lying on the diagonal. Conversely, the more a point is removed from the line, the greater is the disagreement between treatments. In cases where there seemed to be a non-trivial difference between the two treatments, a Spearman rank correlation was used for confirmation. The Spearman rank correlation provides a measure of how similar the rank order is between two ordered lists. For example, if the rank order is A>B>C for both treatments, the results would give a high R and low p-value for the Spearman's test.

Alternatively, if the order is A>B>C for one treatment and C>B>A for the other, we would see a low R and a high p-value. The interpretations between the two treatments could be very different. This test provides one indication of whether differences in treatments will cause differences in interpretation of results, that is, relative station condition.

Total Bioassessment Score. There was no difference in total aggregated metric score between the two taxonomic levels (Figure 5-1) when comparing station rank orders (Spearman rank correlation, R=0.94, p=0.0001).

Metric 1. Taxa Richness. This metric had a value range of 8 to 16 among stations when based on family-level identifications; the value range broadened to 8 to 31 when based on genus/species-level identification. When compared within each station (Figure 5-2), the expected relationship of higher number of taxa for finer taxonomic resolution was observed. For those stations which are in more degraded condition, there was generally a lower magnitude of increase of taxa when identifications were made to the genus/species level. This may illustrate potential partial redundancy with some other metrics (e.g., percent contribution of dominant taxon, HBI, Hydropsychidae/Total Trichoptera). That is, when examining a benthic community at a degraded site, there is often a dominance by few taxa, sometimes one or two. In those cases, the one or two dominant taxa are usually ones with higher tolerance values (as in the Hilsenhoff scheme), thus translating into a higher HBI value (see Metric 2).

Metric 2. Hilsenhoff Biotic Index. Most stations showed little effect of taxonomic levels. However, the HBI is strongly reliant on tolerance values used in its calculation. In some cases, tolerance values were not available for the different taxa at either genus or family level since they are primarily developed for species. In general, however, the largest changes in calculated values were seen for the stations that were in the worst condition overall, with higher HBI values resulting from a more specific taxonomy (Figure 5-3).

Metric 3. Scrapers-Filterer Collectors Ratio. These metric values exhibited large changes when calculated on more specific taxonomic levels. At the family level of identification, the range of values was 0 to 66.7 (Table 5-3), whereas at the genus/species level it was 0 to 52.3 (Table 5-4). Interpretation of this metric is sensitive to two factors: (1) rarity of one of the two functional feeding groups in a sample and (2) increased uncertainty associated with assigning feeding

Table 5-3 Family-level metric values calculated from 100-organism subsamples. Bioassessment scores (in parentheses) are derived by comparing metric values to scoring criteria.

METRIC	CC1	CC2	CC3	HB1	HB2	OC4	OC1	OC2	OC3
1. Taxa richness	14(4)	16(6)	11(4)	9(4)	7(4)	15(6)	10(4)	9(2)	10(4)
2. HBI	4.8(0)	5.5(0)	5.2(0)	4.6(2)	6.3(0)	4.7(2)	6.3(0)	5.5(0)	6.8(0)
3. Scr/(Scr+Fc) x 100	36.6(6)	31.9(6)	22.6(4)	0(0)[a]	0(0)[b]	51.6(4)	25.0(2)	8.6(0)	66.7(6)
4. EPT/(EPT+Chir) x 100	75.9(6)	59.2(6)	88.2(6)	69.7(6)	0(0)	86.4(6)	30.5(2)	60.9(4)	3.6(0)
5. % Contr. Dom. Taxon	30.5(4)	34.7(2)	59.6(0)	70.1(0)	62.4(0)	21.3(4)	49.5(0)	43.1(0)	40.2(0)
6. EPT index	7(4)	5(2)	3(2)	3(2)	0(0)	8(4)	4(2)	1(0)	1(0)
7. (Shred/Tot) x 100	6.8(6)	5.5(6)	1.8(2)	0(0)[c]	0(0)[c]	1.1(4)	0(0)	0.8(4)	0(0)
8. (Hydro/Trich) x 100	92.3(0)	97.9(0)	100(0)	95.2(0)	0(6)[d]	62.5(2)	95.5(0)	100(0)	100(0)
9. Pinkham-Pearson index	UR(6)	6.4(6)	2.7(2)	2(2)	0.1(0)	RR(6)	4.6(6)	4.7(6)	1.0(0)
10. QSI Tax x 100	UR(6)	73(6)	64(6)	16(0)	1(0)	RR(6)	42(6)	46(6)	18(2)
11. DIC-5	UR(6)	3(4)	5(6)	2(2)	1(0)	RR(6)	4.0(6)	4.0(6)	2(2)
12. QSI-FFG x 100	UR(6)	85.6(6)	73.7(6)	49.7(4)	27.6(2)	RR(6)	53.7(6)	66.6(6)	31.1(2)
Total (with paired) metrics	50	50	38	22	12	56	34	34	16
Biology (with paired) % comparison to reference	--	100	76	44	24	--	61	61	28
Total (without paired) metrics	26	28	18	14	10	32	10	10	10
Biology (without paired) % comparison to reference	--	108	69	54	20	--	31	31	31
Habitat Score	139	132	92	182	57	191	86	114	118
Habitat % comparison to reference	--	95	66	131	41	--	45	60	62

UR = Upstream Reference; RR = Regional Reference; CC1 also served as reference for Harbor Brook, see page 4-11 for further discussion.
[a] No scrapers
[b] No scrapers or filterer-collectors
[c] No shredders
[d] No Trichoptera

designations, which are usually assigned to species, to higher taxonomic levels. The is because (1) many invertebrate taxa are poorly known and (2) some taxa are known to shift feeding behavior upon entering subsequent developmental life stages.

Metric 4. EPT-Chironomidae Ratio. There is no effect on this metric since it is based on the number of individuals in these taxonomic groups (family and order, not genus/species).

Metric 5. Percent Contribution of Dominant Taxon. When taxonomic groups are split (as accomplished by more specific taxonomy), there are fewer individuals representative of each of the subgroups and an overall lower contribution to sample composition. In sites considered to be in better condition, values for this metric would thus be expected to substantially decrease with more specific levels of taxonomy. However, this expectation was not consistent with some of the results (Table 5-4, Figure 5-4). Station OC4, the regional reference

Table 5-4 Genus/species-level metric values calculated from 100-organism subsamples. Bioassessment scores (in parentheses) are derived by comparing metric values to scoring criteria.

METRIC	CC1	CC2	CC3	HB1	HB2	OC4	OC1	OC2	OC3
1. Taxa richness	24(4)	31(6)	17(2)	13(2)	11(2)	26(6)	28(6)	19(4)	16(4)
2. HBI	4.4(2)	5.2(2)	5.0(2)	5.9(2)	8.5(0)	4.4(2)	6.0(0)	5.6(0)	7.0(0)
3. Scr/(Scr+Fc) x 100	36.7(6)	21.7(4)	16.7(2)	0(0)	0(0)[b]	52.3(6)	3.1(0)	0(0)	0(0)
4. EPT/(EPT+Chir) x 100	75.9(6)	59.2(4)	88.2(6)	69.7(6)	0(0)	86.4(6)	30.5(2)	60.9(4)	3.6(0)
5. % Contr. Dom. Taxon	27.5(4)	13.1(6)	25.7(4)	70.1(0)	58.1(0)	20.2(0)	12.4(4)	17.9(0)	22(2)
6. EPT index	9(6)	8(4)	6(4)	5(2)	0(0)	13(6)	6(2)	4(2)	1(0)
7. (Shred/Tot) x 100	9.3(6)	9.1(6)	5.5(4)	5.8(4)	0.9(0)	4.3(0)	9.5(2)	13(4)	19.7(6)
8. (Hydro/Trich) x 100	92.3(0)	97.9(0)	100(0)	95.2(0)	(0)(6)[a]	62.5(2)	95.5(0)	100(0)	100(0)
9. Pinkham-Pearson index	UR(6)	7.8(6)	3.3(2)	2.0(2)	0.1(0)	RR(6)	5.1(4)	8.3(6)	0.7(0)
10. QSI Tax x 100	UR(6)	46(6)	55(6)	16(2)	1(0)	RR(6)	22(4)	34(6)	10(2)
11. DIC-5	UR(6)	2(4)	2(4)	2(4)	0(0)	RR(6)	0(0)	1(2)	0(0)
12. QSI-FFG x 100	UR(6)	82.2(6)	72.9(6)	49.7(4)	27.6(2)	RR(6)	60.3(6)	62.8(6)	30.6(4)
Total (with paired) metrics	58	54	42	28	10	52	30	34	18
Biology (with paired) % comparison to reference	48	93	76	--	17	--	58	65	35
Total (without paired) metrics	34	32	24	16	8	28	16	14	12
Biology (without paired) % comparison to reference	--	94	71	47	23	--	57	50	43
Habitat score	139	132	92	182	57	191	86	114	118
Habitat % comparison to reference	--	95	66	131	41	--	45	60	62

UR = Upstream Reference; RR = Regional Reference; CC1 also served as reference for Harbor Brook, see page 4-11 for further discussion
[a] No scrapers
[b] No scrapers or filterer-collectors

site on the West Branch Tioughnioga River, only changed from 21 percent (family-level) to 20 percent (genus/species-level). Conversely, the farthest downstream station on Canastota Creek, which exhibited moderate impairment, decreased from 60 to 27 percent.

Metric 6. EPT Index. Because this metric is a restricted form of taxonomic richness, a similar general response to level of identification is expected. Small increases in this value are seen with genus/species-level taxonomy (Tables 5-3, 5-4).

Metric 7. Shredders/Total No. Individuals. There is minimal effect on this metric except where families are not designated as shredders and genera or species are designated.

Metric 8. Hydropsychidae/Total Trichoptera. There is no effect on this metric since it is based on the number of individuals in these two taxonomic groups only.

Metric 9. Pinkham-Pearson Community Similarity Index. The effect of taxonomic level on this metric was minimal (Figure 5-5). Values ranged from 0.1 to 6.4 for family-level identifications and from 0.1 to 8.3 for genus/species-level identification. The middle station on Onondaga Creek (OC2) had a value shift from 4.7 to 8.3, the largest change by far.

Metric 10. Quantitative Similarity Index-Taxa. The effect of more specific taxonomy was minimal, as indicated by a high correlation of rank orders (Spearman rank correlation, R=0.93, p=0.002) between the two treatments. The largest difference in values was observed at Station OC1 with a family-level value of 42 and a genus/species-level of 22.

Metric 11. Dominants-in-Common-5. A minimal range of possible values for this metric makes it difficult to interpret. An example of unpredictable changes in this metric is illustrated at Stations OC1 and OC3, where the DIC value fell from 4 to 0 and 2 to 0, respectively, when the calculation was done at the generic level. At both stations, there were dominant, family-level taxa in common but they were represented by different genera, thus accounting for the lower DICs. When subjected to the two treatments, there was a relatively low correlation of rank orders (Spearman R=0.35, p=0.44); therefore, taxonomic treatments could lead to different comparisons between stations for this metric.

Metric 12. Quantitative Similarity Index-Functional Feeding Group. There were only minor changes in values when calculated at family versus genus/species level. Any differences were probably due to differential availability of functional feeding group designations among the taxonomic levels. However, rank order correlations showed no difference with a Spearman rank correlation R of 1.0.

5.2.2 Subsampling Level Effects on Metric Performance

RBPs provide a mechanism for substantially reducing the level of effort through randomized subsampling. The comparisons presented here illustrate the behavior of identical metrics when calculated on differential subsampling intensities. Using metric values calculated at the taxonomic level of genus/species, the effect of subsample size on metric performance was evaluated. Comparisons of RBPIII with subsampling at the 100-organism (Table 5-4) and 300-organism (Table 4-3) levels were done through a combination of correlational scatterplots and confirmation of differences with Spearman rank correlations.

A previous unpublished study (Stribling and Gerardi 1993 [draft report]) has shown that two metrics are strongly biased by different organism counts, taxa richness and EPT index, showing a marked increase with higher numbers of individuals. However, two factors diminish the importance of these biases. First, the relationship is a predictable one; second, metrics used in RBP site assessments are evaluated based on their value relative to reference conditions rather than on absolute numbers. Thus, if data representing reference sites or conditions are collected in the same manner, these biases become essentially irrelevant. The following analyses provide further confirmation of these conclusions, including those concerning minimal effects on the other metrics.

Total Bioassessment Score. Overall bioassessment score is not affected by differential subsample sizes (Figure 5-6); rank order correlation is perfect (R=1.00).

Metric 1 Taxa Richness. This metric had a value range of 8 to 31 taxa at the 100-organism subsample and 16 to 41 at the 300-organism subsample (Figure 5-7). Number of taxa increases significantly as larger samples are analyzed, but correlation of rank orders is nearly perfect (Spearman R=0.95, p=0.000066). Therefore, a larger sample size would not affect comparisons between stations when using this metric.

Metric 2 Hilsenhoff Biotic Index. Subsampling level had no effect on the HBI values with a nearly 1:1 correlation (Spearman R=0.99, p=0.00) between the two treatments.

Metric 3 Scraper-Filterer Collector Ratio. Although somewhat more variable, rank orders show significant correlation for the subsample size (Spearman R=0.93, p=0.0003) (Figure 5-8). Therefore, subsample size had no effect on station comparisons using this metric. No scrapers were selected in the 100-organism subsample at HB1, which caused the metric to have a value of 0; one scraper was selected in the 300-organism subsample giving a value of 16.7.

Metric 4 EPT-Chironomidae Ratio. Subsample size had no effect on the results calculated from this metric (Spearman R=0.92, p=0.0005).

Metric 5 Percent Contribution of Dominant Taxon. Subsample size had no effect on the values calculated for this metric (Spearman R=1.0).

Metric 6 EPT Index. As seen for taxa richness (Metric 1), a difference was detected for this richness metric, but there was no difference in rank orders (Spearman R=0.98, p=0.000002) of the samples. The number of EPT taxa increases as larger samples are taken, especially at less degraded sites, due to the sensitivity of the species.

Metric 7 No. Shredders/Total Sample. Similarly to the Scraper-Filterer Collector Ratio, this functional feeding group metric appears more variable, but differences in rank orders are nonsignificant (Spearman R=0.97, p=0.00002) (Figure 5-9). Different subsample sizes have no effect on interpretations using this metric. By chance, we got a higher percentage of shredders in the 100-organism subsample (19.7 versus 15.8 for the 300-organism subsample).

Metric 8 Hydropsychidae/Total Trichoptera. This metric is not significantly affected by different subsample sizes (Spearman R=0.97, p=0.000014).

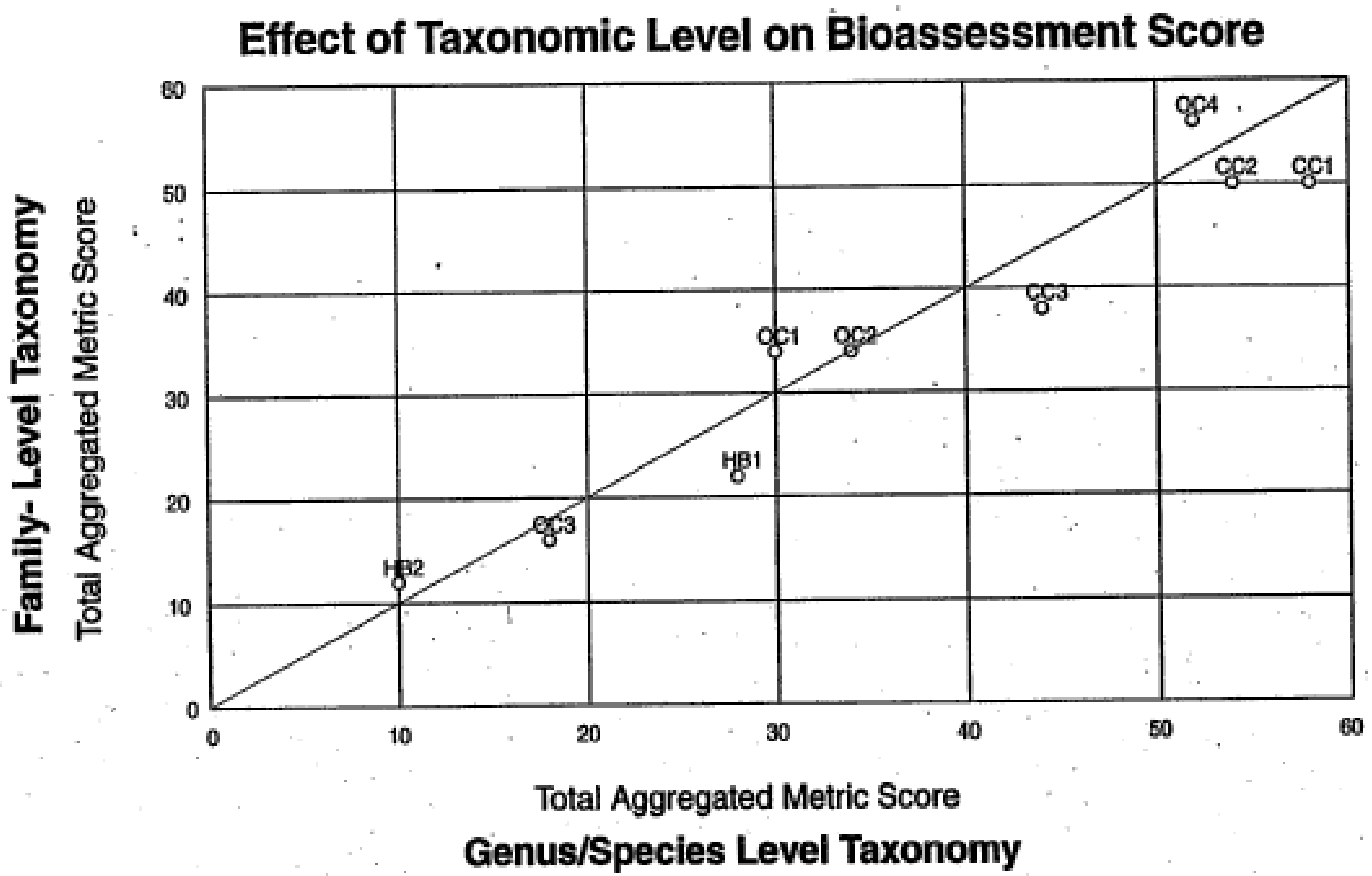

Figure 5-1. Correlational scatterplot (1:1) total bioassessment score, family vs. genus/species-level taxonomy.

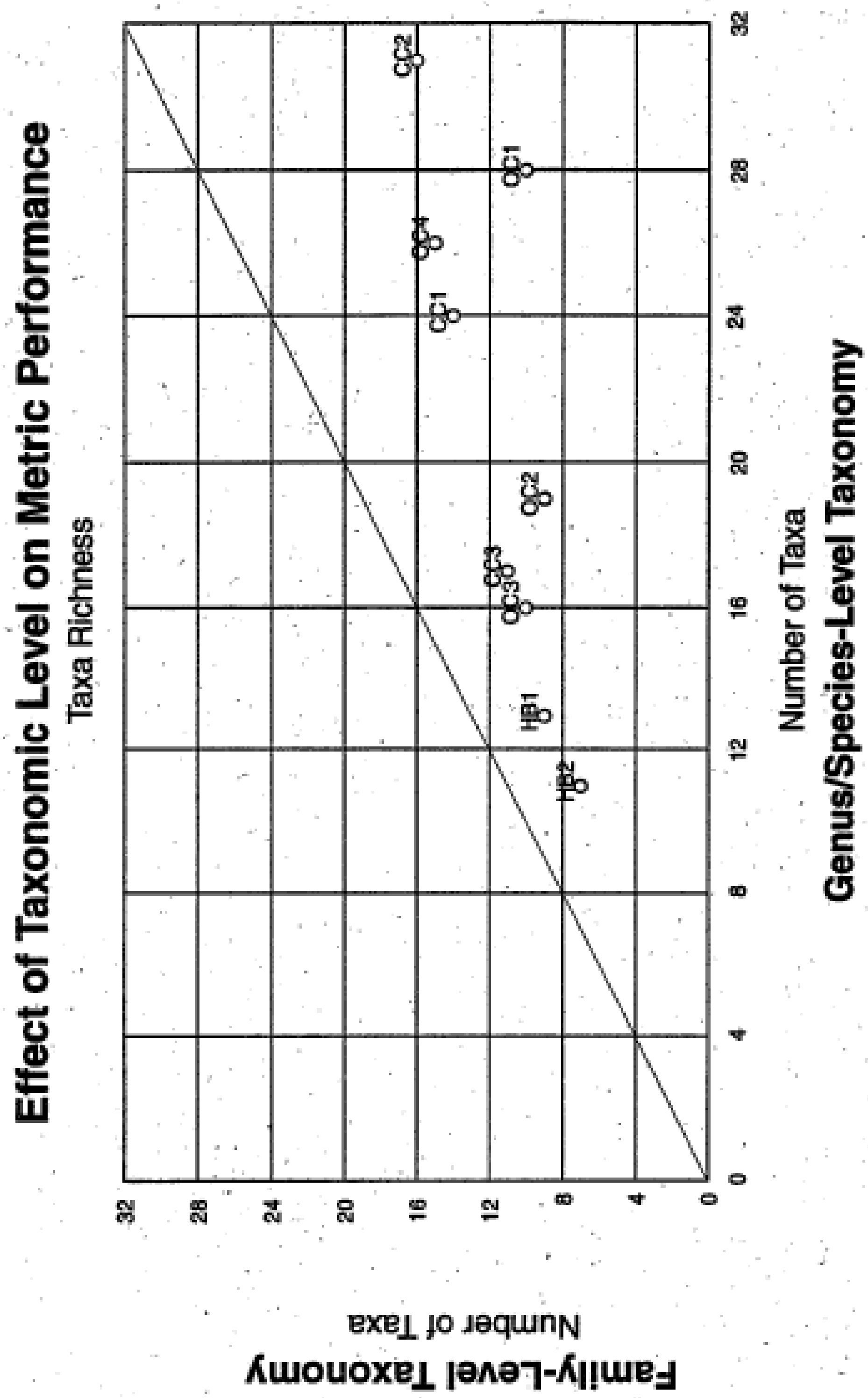

Figure 5-2. Correlational scatterplot (1:1) of taxa richness, family vs. genus/species-level taxonomy.

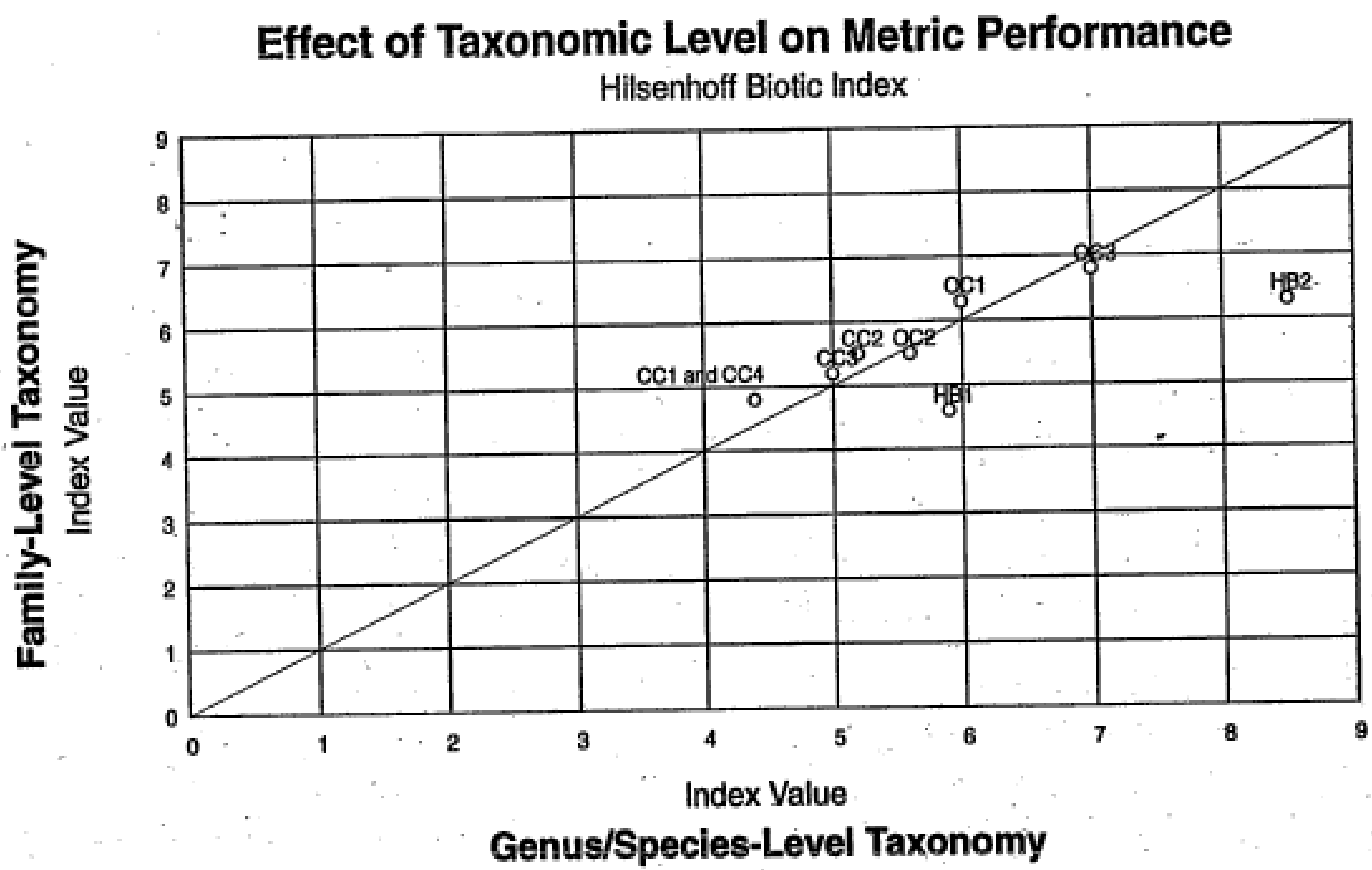

Figure 5-3. Correlational scatterplot (1:1) of the Hilsenhoff Biotic (HBI) values, family vs. genus/species-level taxonomy. Note: Stations CC1 and OC4 share the same coordinates.

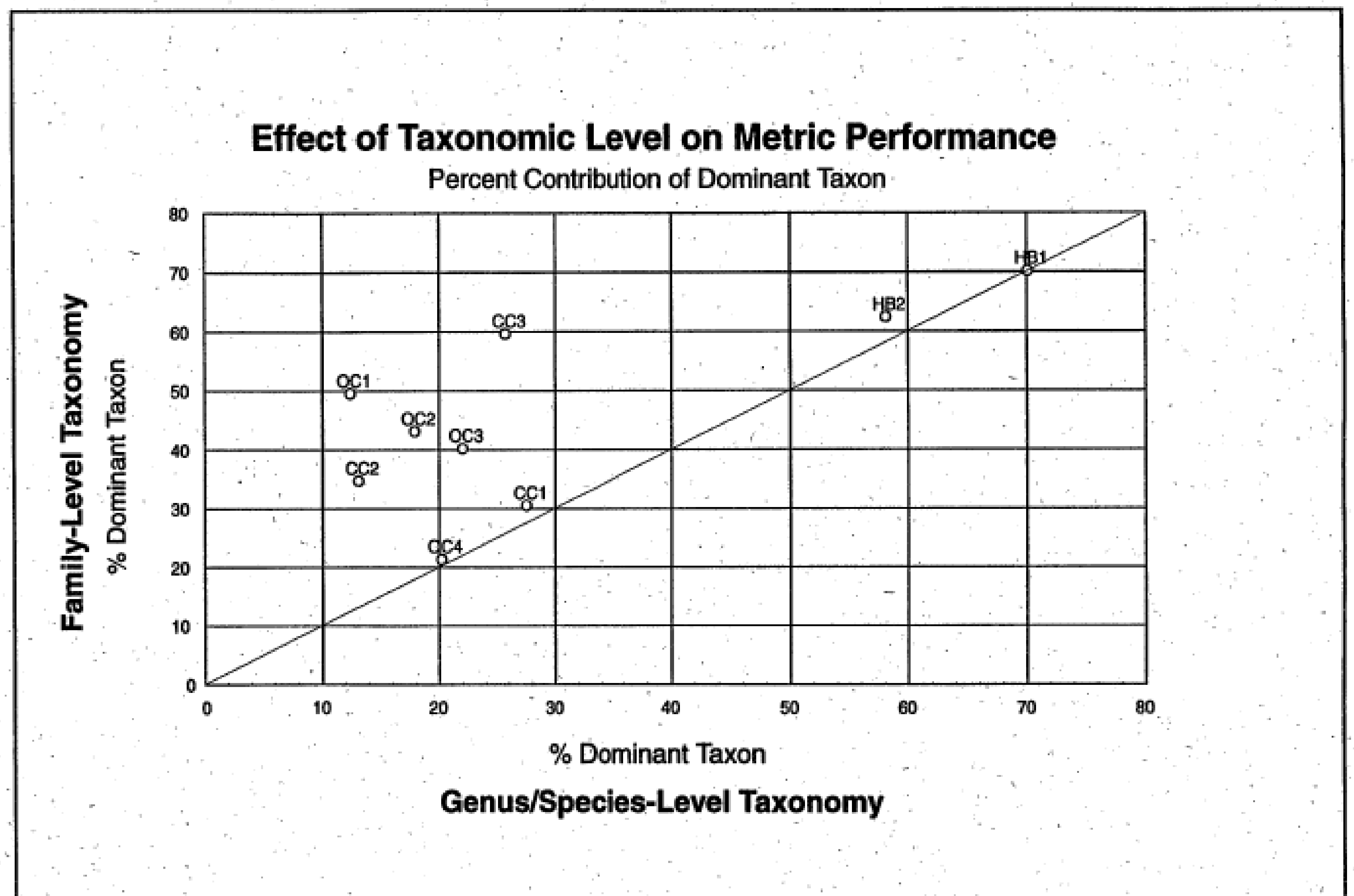

Figure 5-4. Correlational scatterplot (1:1) of percent contribution of dominant taxon, family vs. genus/species-level taxonomy.

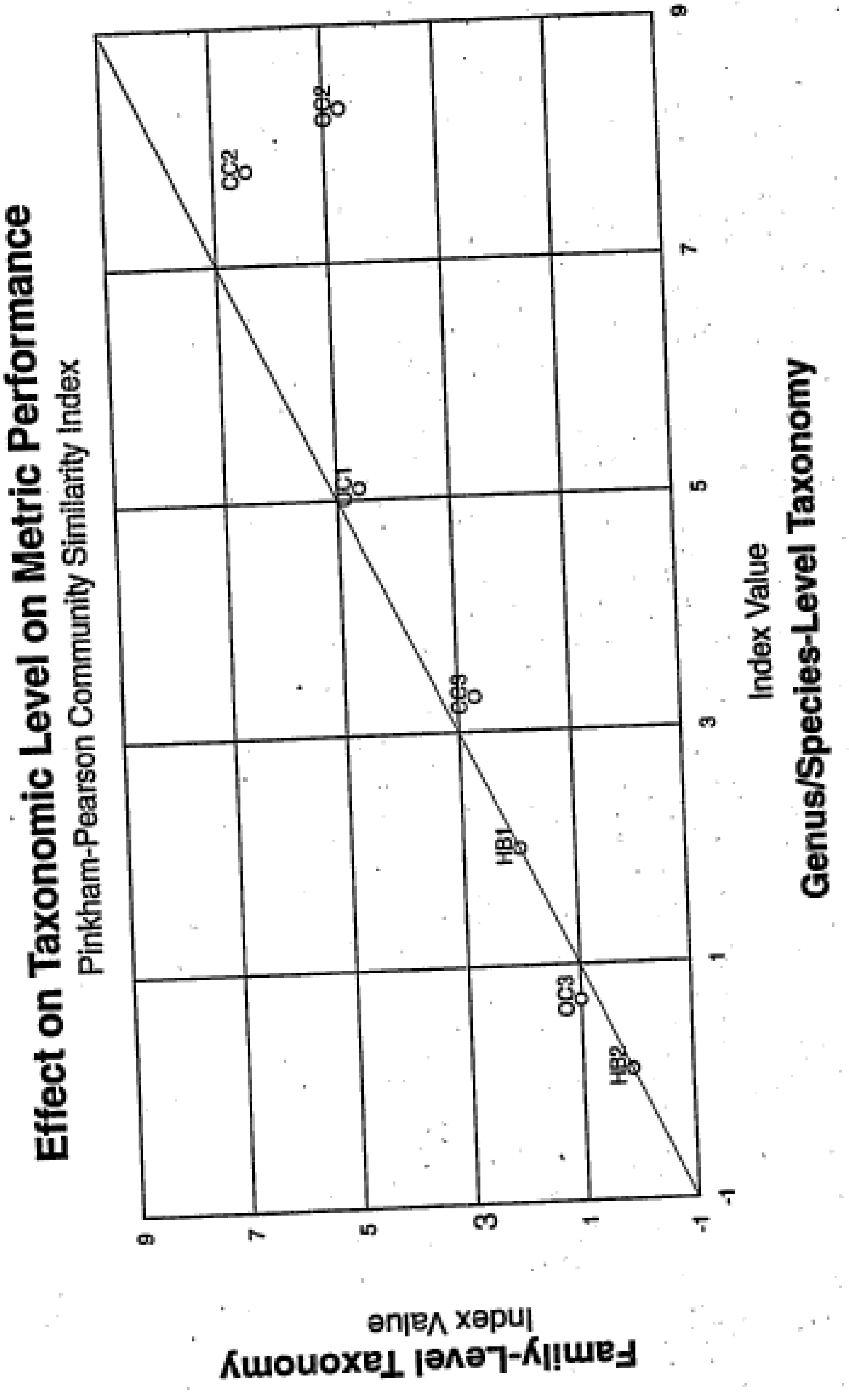

Figure 5-5. Correlational scatterplot (1:1) of Pinkham-Pearson Community Index, family vs. genus/species-level taxonomy.

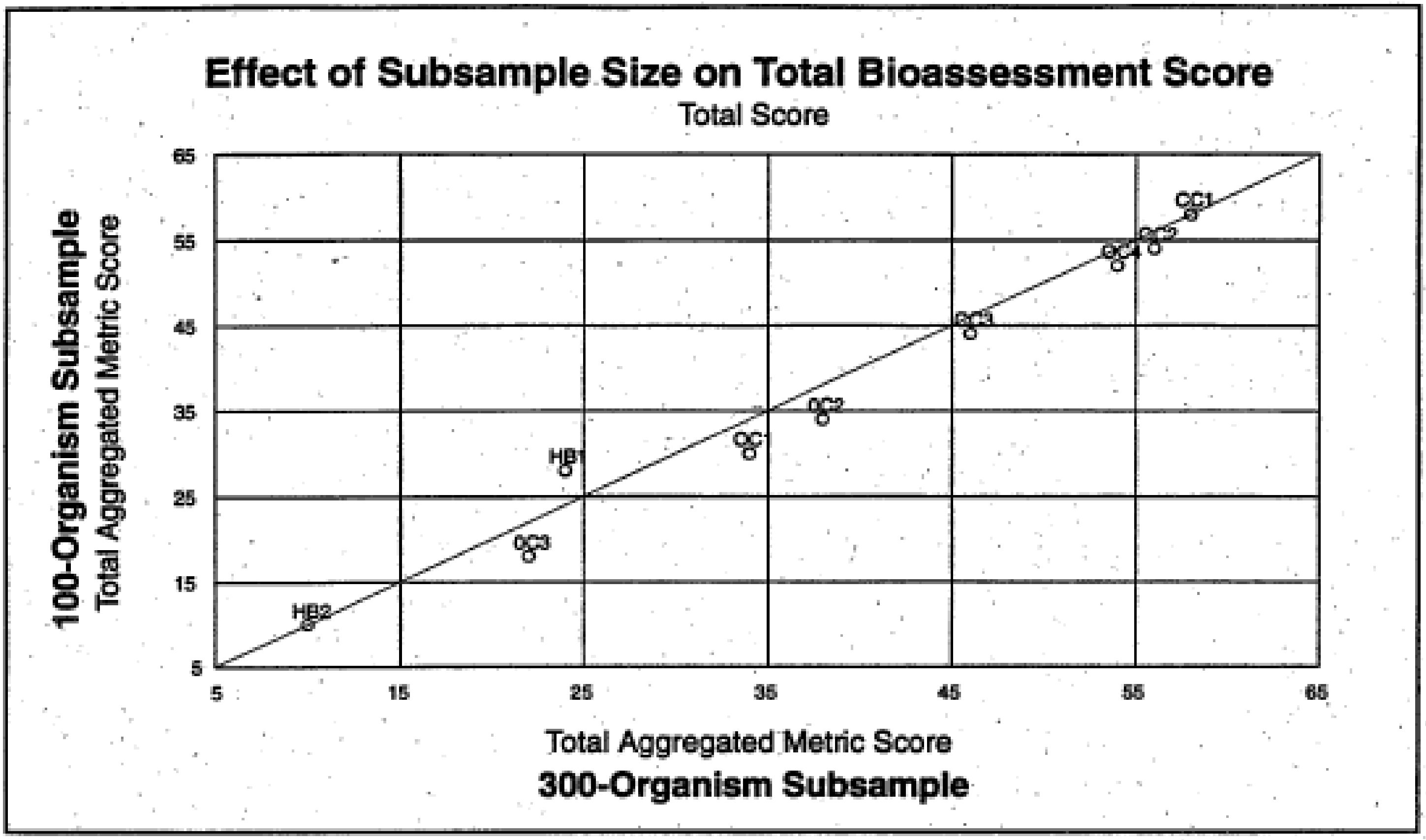

Figure 5-6. Correlational scatterplot (1:1) of bioassessment score, 100 vs. 300 organism subsample.

Metric 9 Pinkham-Pearson Community Similarity Index. This metric appears to be more variable with differential subsample size, but differences are nonsignificant in comparison of rank orders (Spearman R=0.92, p=0.0025).

Metric 10 Quantitative Similarity Index-Taxa. Different subsample sizes have little effect on this metric and differences in values are shown to be nonsignificant (Spearman R=0.93, p=0.0025).

Metric 11 Dominants-in-Common-5. This metric does not seem to be affected by subsample size, but similar to the analysis of differential taxonomic levels, correlated variation is difficult to determine due to a narrow range of possible values. Because it is common to have several ties in a small data set such as this, ordinal analyses such as Spearman rank correlation can have diminished meaning. Station CC1 was used as the upstream reference; the other stations for which this was used as a baseline had no changes in value (HB1 and HB2) or changed by only one (CC2 and CC3). For the OC4-compared stations, there were no changes in metric values with higher levels of subsampling.

Metric 12 Quantitative Similarity Index-Functional Feeding Group. This metric is not affected by subsample size; there is a perfect rank order correlation (Spearman R=0.96, p=0.0004).

5.3 Summary of Results

These comparisons have shown that there are some effects on metric behavior when subjected to different treatments. For taxonomic level, five metrics (taxa richness, HBI, scraper-filterer collector ratio, percent contribution of dominant taxon, and shredders-to-total ratio) were found to be substantially different; for another seven, there was either perfect 1:1 correlation or nearly perfect. For the different subsampling levels, only two metrics performed differently between higher and lower levels of organisms: taxa richness and EPT index. For both sets of treatments, total bioassessment scores were not affected, with essentially perfect agreement between them. Refer to Section 6.2 for further discussion.

The screening-level assessment (RBPI) proved to be a useful tool for identifying sites with biological impairment. One site was screened as minimally impaired and was further assessed, using RBPIII, as having severe impairment.

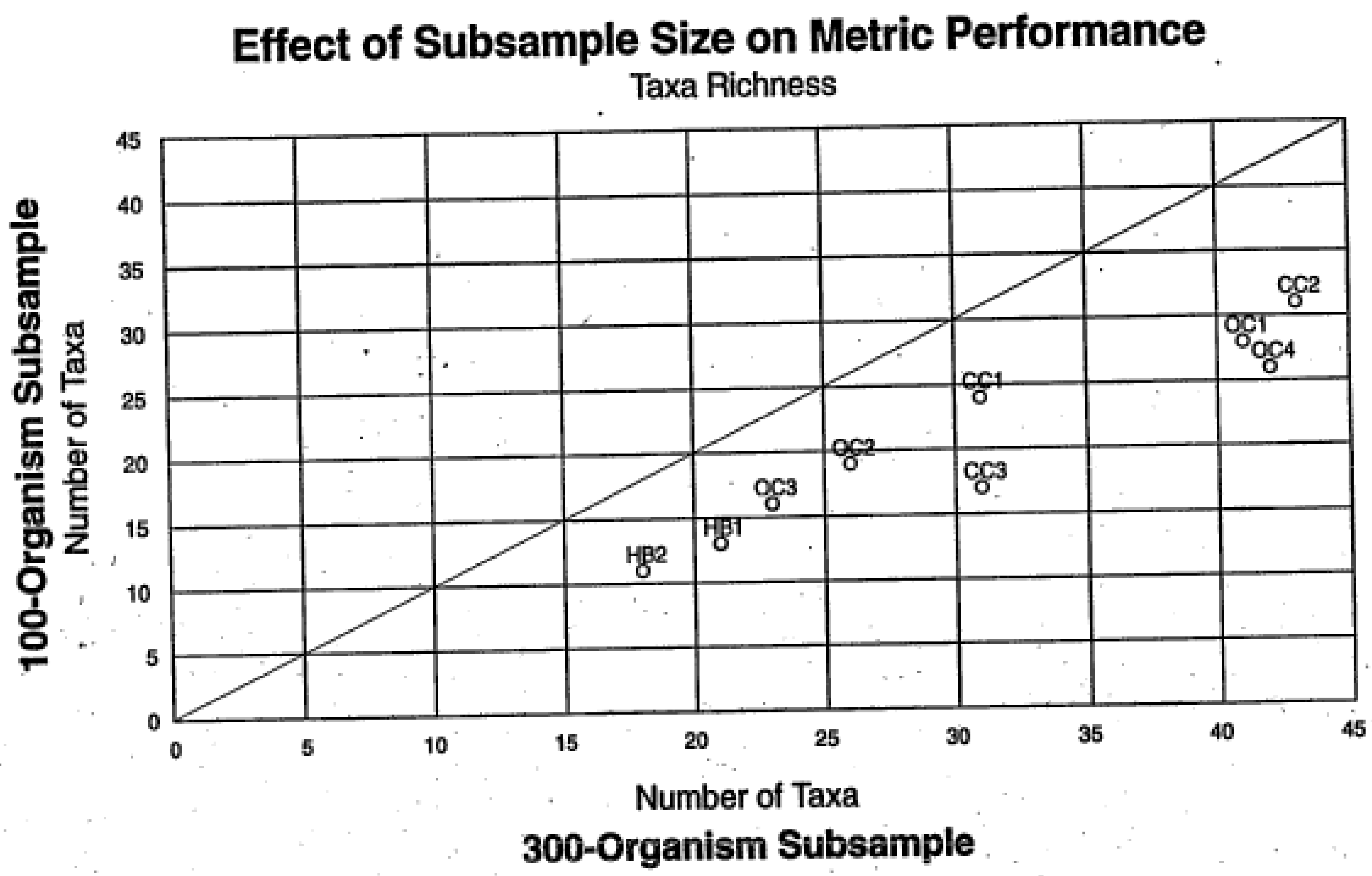

Figure 5-7. Correlational scatterplot (1:1) of taxa richness, 100 vs. 300 organism subsample.

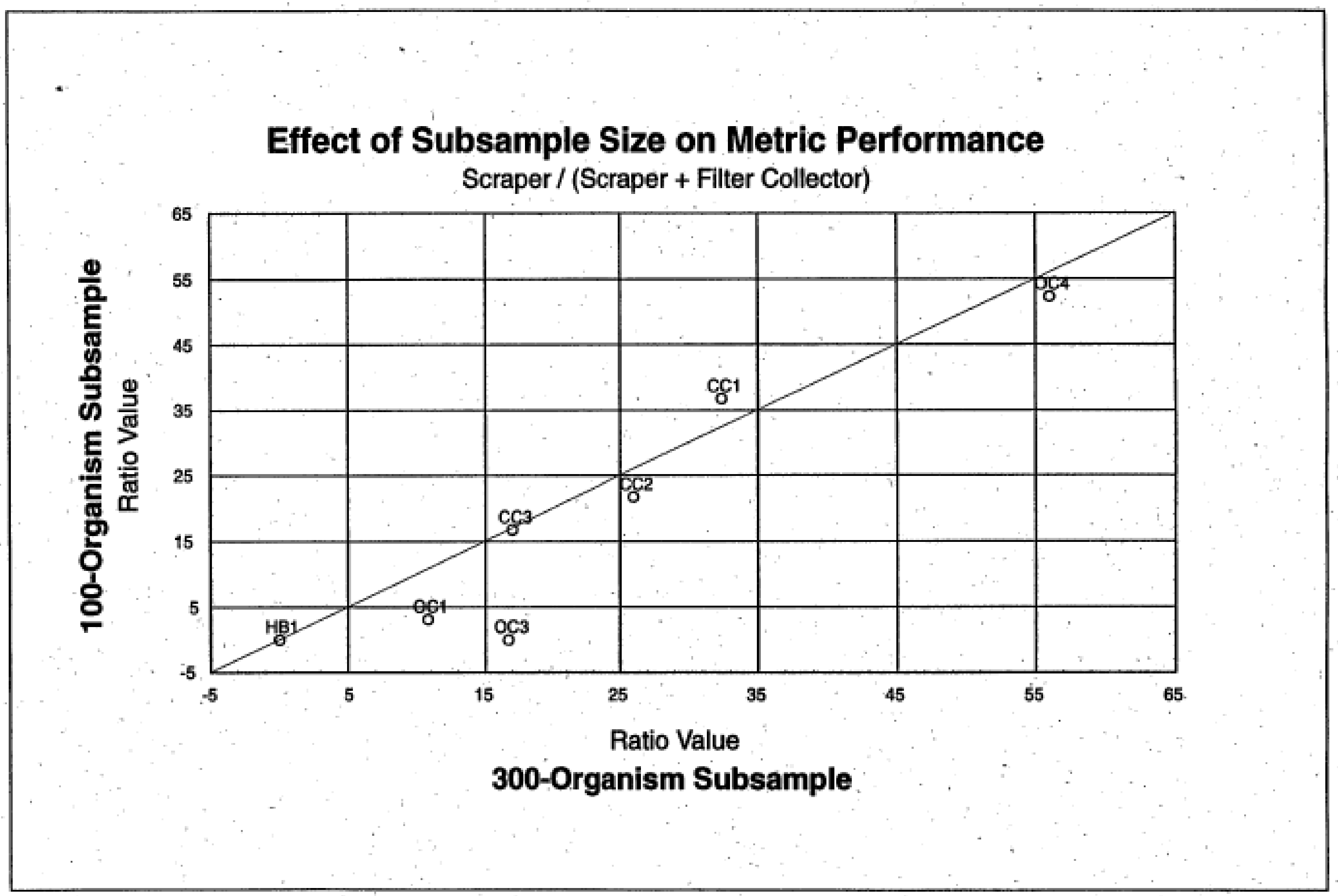

Figure 5-8. Correlational scatterplot (1:1) of Scraper/(Scraper + Filter Collector, 100 vs. 300 organism subsample.

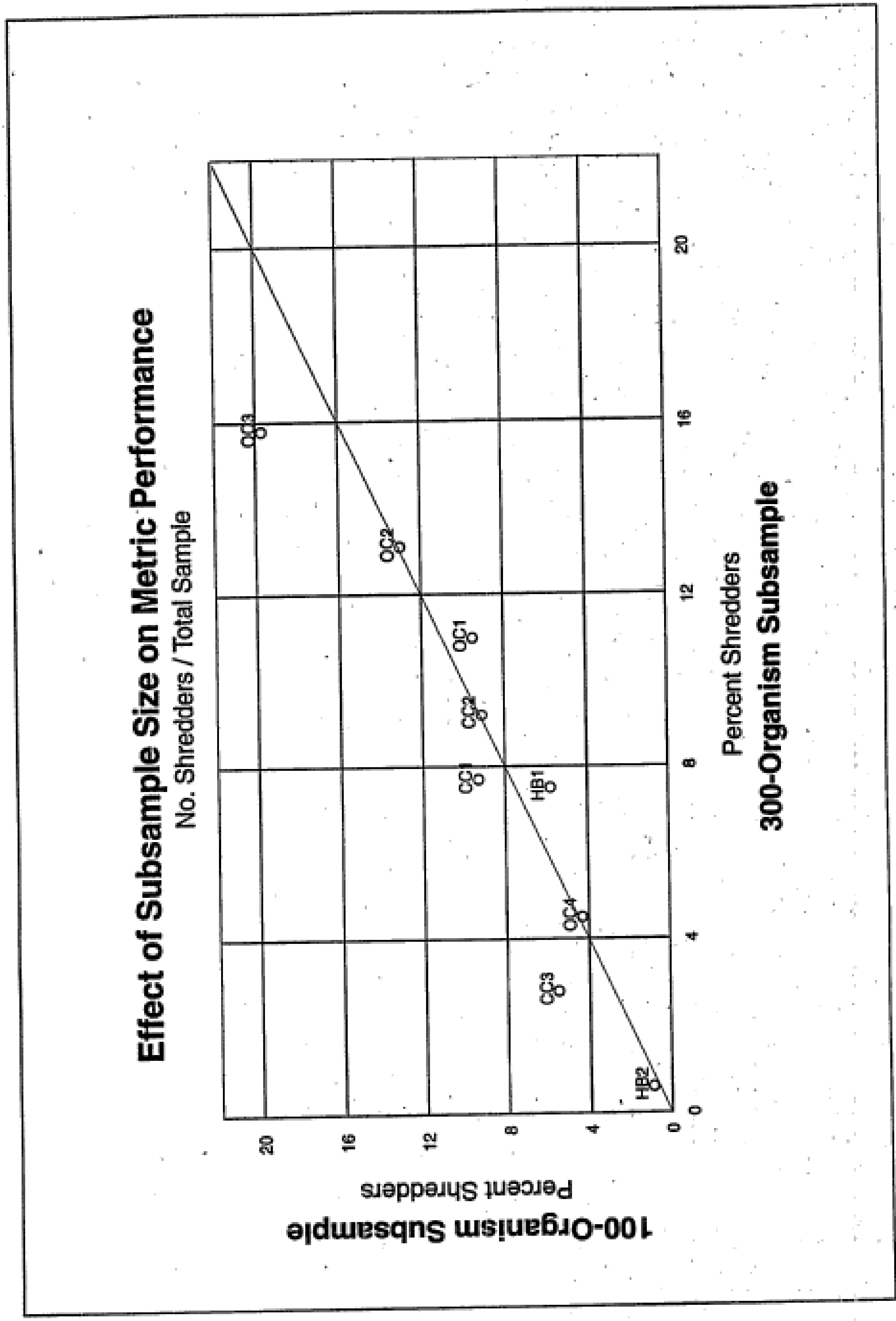

Figure 5-9. Correlational scatterplot (1:1) of No. Shredders/Total Sample, 100 vs. 300 organism subsample.